At page 49, Table 3, kindly delete lines 7-12 with the following:

--Parent	GWYAL (SEQ ID NO: 24)	0.0203	-
B1B3	VNLLV (SEQ ID NO: 25)	0.0233	0.87
B1F12	RSMDG (SEQ ID NO: 26)	0.0283	0.71
B2B4	HAARR (SEQ ID NO: 27)	0.0113	1.79
B2H1	RVRLL (SEQ ID NO: 28)	5.9e-3	3.44
B2B3	FLSSI (SEQ ID NO: 29)	0.0228	0.89--

At page 49, Table 4, kindly delete lines 25-30 with the following:

--Parent	DSSGN (SEQ ID NO: 30)	0.0203	-
C5	SATHE (SEQ ID NO: 31)	0.0166	1.2
C10	APHGS (SEQ ID NO: 32)	0.0144	1.4
A12	TVNHD (SEQ ID NO: 33)	0.0104	2.0
D1	HWQTD (SEQ ID NO: 34)	7.4e-3	2.7
H7	NTSVT (SEQ ID NO: 35)	2.5e-3	8.12--

IN THE DRAWINGS:

Please replace Fig. 2B with the attached revised Fig. 2B, which has been amended to show the sequence identification number.

REMARKS

The present amendment incorporates the sequence identifiers in the specification and drawings. These are the only changes made to the specification and no new matter has been added. Also, substitute pages 30, 32-33, 36-37, 42 and 49 of the specification are enclosed herewith for the convenience of the Examiner. Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "**Appendix. Version with Markings to Show Changes Made.**"

Please charge (or credit) any fees associated with this response to the firm's Deposit Account No. 20-1430. If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 206-467-9600.

Respectfully submitted,

Dated: July 24, 2001

By: Steven W. Parmelee
Steven W. Parmelee
Reg. No. 31,990

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SE 5009254 v1

APPENDIX
Version with Markings in Bold Print to Show Changes Made

IN THE SPECIFICATION:

Kindly replace page 30, with the following rewritten page:

min. The pull through reaction is a PCR that uses primers which are at the extreme ends of the two DNA fragments being annealed in the assembly reaction. In this way, full length assembled product is amplified from the fragment mixture. An assembled product of the expected size (1.1 kb) was produced and gel purified. This product can be used directly as starting template for a coupled *in vitro* translation/transcription reaction.

Primers used (all written 5'-3'):

PEU **(SEQ ID NO: 2)**
AA TTC TAA TAC GAC TCA CTA TAG GGA GAG CAC TTC TGA TCC AGT CCG ACT GAG AAG GAA GGC CCA GCC GGC CAT GG

HA TAG **(SEQ ID NO: 3)**
TAC CCG TAT GAC GTG CCG GAT TAC GCA

T7 **(SEQ ID NO: 4)**
TAA TAC GAC TCA CTA TAG GGA GAG CAC TTC TG

HA mini **(SEQ ID NO: 5)**
TGC GTA ATC CGG CAC

Mycseq 10 **(SEQ ID NO: 6)**
CTC TTC TGA GAT GAG TTT TTG

Hismyc back **(SEQ ID NO: 7)**

GCA CAT CAT CAT CAC CAT CAC GGG GCC

c) Characterisation of the PCR assembled library on the basis of scFv expression

The scFv repertoire assembled with a glycine-serine tether was

At page 32 on lines 22-31, kindly replace paragraphs 3 and 4 with the following rewritten paragraphs:

HA-OAS 1 (135mer) (5'-3') **(SEQ ID NO: 8)**:

TGC GTA ATC CGG CAC GTC ATA CGG GTA ACT ATT TTT CCC TTT GCG GAC ATC ACT CTT TTT TCC GGT TCG AGA TCG AAA CTT TGC AAG CCT GAT CGA CAT AGG GAC ATC TTC CAT GAA CTC ATC AAC GAC TTC TTC

HA-OAS 2 (no stop) (144mer) (5'-3') **(SEQ ID NO: 9)**:

GAA CTC ATC AAC GAC TTC TTC TGT AAG TTC CAT GGG CCC TCC GTC TCT CAC GTT TGT AAT CTT CTC TCT CAA ACC ATT CAG ATC CTC TTC TGA GAT GAG TTT TTG TTC TGC GGC CCC GTG ATG GTG ATG ATG ATG TCG GGC CGC

At page 33, at line 6, kindly replace paragraph 2 with the following rewritten paragraph:

HA-OAS 2 stop (5'-3') **(SEQ ID NO: 10)**:

GAA CTC ATC AAC GAC TTC TTC TGT AAG TTC CAT GGG CCC TCC GTC TCT CAC GTT TGT AAT CTT CTC TCT CAA ACC CTA ATT CAG ATC CTC TTC TGA GAT GAG TTT TTG TTC TGC GGC CCC GTG ATG GTG ATG ATG ATG TCG GGC CGC

At page 36, at lines 12-24, kindly replace paragraphs 3 and 4 with the following rewritten paragraphs:

The MVD1 replication site includes 63 nucleotides at the 5= end of the construct as follows (5'-3'): GGGGACCCCCCCGGAAGGGGGGGACGAGGTGCGGGCACCTCGTACGGGAG TTCGACCGTGACG **(SEQ ID NO: 11)**.

This 63 nucleotide segment is then followed by the expression unit containing the scFv gene segments, detection and purification tags, the TMV OAS sequence if required and a tether. The 3' end of the construct then includes the 3' MDV sequence that is 156 nucleotides long as follows (5"-3'):CACGGGCTAGCGCTTTCGCGCTCTCCCAGGTGACGCCTCGTGAA GAGGCGCGACCTTCGTGCGTTTCGGTGACGCACGAGAACCGCCACGCTGCTTCGC AGCGTGGCTCCTTCGCGCAGCCCGCTGCGCGAGGTGACCCCCCGAAGGGGGGTTC CC **(SEQ ID NO: 12)**.

Kindly replace page 37, with the following rewritten page:

(5'-3').

GGGGACCCCCCCGGAAGGGGGGGACGAGGTGCGGGCACCTCGTACGGGAGTTCG ACCGTGACGAATTCTAATACGACTCACTATAG **(SEQ ID NO: 13)**

MDV2: HA detection tag (bold face) followed by the first 79 nucleotides of the 3= segment of the MDV RNA.

Sense

TACCCGTATGACGTGCCGGATTACGCACACGGGCTAGCGCTTTCGCGCTCTCCCAG GTGACGCCTCGTGAAGAGGCGCGACCTTCGTGCGTTTCGGTGACGCACGA **(SEQ ID NO: 14)**

Reverse complement (5'-3')

TCGTGCGTCACCGAAACGCACGAAGGTCGCGCCTCTTCACGAGGCGTCACCTGGG
AGAGCGCGAAAGCGCTAGCCCGTGTGCGTAATCCGGCACGTCATACGGGTA **(SEQ ID NO: 15)**

MVD3: Remaining 77 nucleotides of the 3' MDV segment within an additional 19 nucleotide overlap (bold face) with MDV2 to allow assembly.

Sense

GCGTTTCGGTGACGCACGAGAACCGCCACGCTGCTTCGCAGCGTGGCTCCTTCGCG
CAGCCCGCTGCGCGAGGTGACCCCCCGAAGGGGGGTTCCC **(SEQ ID NO: 16)**

Reverse complement

GGGAACCCCCCTTCGGGGGGTCACCTCGCGCAGCGGGCTGCGCGAAGGAGCCACG
CTGCGAAGCAGCGTGGCGGTTCTCGTGCGTCACCGAAACGC **(SEQ ID NO: 17)**

b) Assembly conditions

At page 42, lines 2 and 3, kindly replace both lines with the following:

VH CDR3 NMVRGVGRYYYMDV **(SEQ ID NO: 18)**

VL CDR3 CSRDSSGYHLV **(SEQ ID NO: 19)**

At page 42, lines 20-23, kindly replace paragraphs 6 and 7 with the following rewritten paragraphs:

The VH CDR3 of the parent had the following sequence: VHNGWYALEY **(SEQ ID NO: 20)**.

The VL CDR3 of the parent had the following sequence: NSWDSSGNHVV **(SEQ ID NO: 21)**.--

At page 42, lines 31-33, kindly replace paragraphs 10 and 11 with the following rewritten paragraphs:

Library H4 (VH CDR3) VHNXXXXXEY **(SEQ ID NO: 22)**

Library L4 (VL CDR3) NSWXXXXXHVV **(SEQ ID NO: 23)**

At page 49, Table 3, kindly delete lines 7-12 with the following:

Parent	GWYAL **(SEQ ID NO: 24)**	0.0203	-
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